

## SEQUENCE LISTING

<110> Agency for Science, Technology and Research

<120> Protein Separation Device

<130> 51571-4

<150> US 60/530,608

<151> 2003-12-19

<160> 8

<170> PatentIn version 3.3

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<211> 1647

<212> DNA

<213> Escherichia coli

<220>

<221> misc\_feature

<223> GroEL wildtype DNA sequence

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&lt;212&gt; PRT

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&lt;223&gt; GroEL wildtype amino acid sequence

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35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp  
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Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys  
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Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala  
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Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn  
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Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp  
210 215 220

Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val  
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Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly  
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Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys  
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 Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln  
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 485 490 495  
 Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly  
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&lt;211&gt; 1647

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

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 <223> GroEL-Asp490Cys DNA sequence

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 <222> (1468)..(1470)  
 <223> GAC to TCG

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 <212> PRT  
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 35 40 45  
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 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys  
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 Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala  
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 405 410 415  
 Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln  
 420 425 430  
 Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu  
 435 440 445  
 Ala Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val  
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 Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala  
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 <223> GAC to TGC

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<213> Escherichia coli

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35 40 45

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 Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn  
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 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Val Ala Val  
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 Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys  
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 Met Gln Phe Asp Arg Gly Tyr Arg Tyr Asp Tyr Phe Ile Asn Lys Pro  
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 Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp  
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 Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val  
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 Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys  
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 Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met  
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 Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val  
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 Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln  
 340 345 350  
 Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg  
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Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala  
 370 375 380  
 Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu  
 385 390 395 400  
 His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly  
 405 410 415  
 Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln  
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 Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu  
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 Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala  
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 Ala Thr Glu Glu Tyr Gly Asn Met Ile Cys Met Gly Ile Leu Asp Pro  
 485 490 495  
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<210> 7  
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<222> (787)..(792)

<223> GTTGTT to CTTTTC

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Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
35          40          45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
50          55          60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65          70          75          80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
85          90          95

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Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn  
 100 105 110  
 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val  
 115 120 125  
 Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile  
 130 135 140  
 Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys  
 145 150 155 160  
 Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr  
 165 170 175  
 Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly  
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 Met Gln Phe Asp Arg Gly Ile Leu Ser Pro Ile Phe Ile Asn Lys Pro  
 195 200 205  
 Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp  
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 Lys Lys Ile Ser Asn Ile Arg Glu Met Ile Pro Val Ile Glu Ala Val  
 225 230 235 240  
 Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly  
 245 250 255  
 Glu Ala Phe Ala Thr Leu Leu Phe Asn Thr Met Arg Gly Ile Val Lys  
 260 265 270  
 Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met  
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 Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala  
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 Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val  
 325 330 335  
 Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln  
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 355 360 365  
 Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala  
 370 375 380  
 Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu  
 385 390 395 400  
 His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly  
 405 410 415

Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln  
420 425 430

Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu  
435 440 445

Ala Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val  
450 455 460

Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala  
465 470 475 480

Ala Thr Glu Glu Tyr Gly Asn Met Ile Cys Met Gly Ile Leu Asp Pro  
485 490 495

Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly  
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Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp  
515 520 525

Ala Ala Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met  
530 535 540

Gly Gly Met Met  
545